

SEQUENCE LISTING

<110> Innovations Foundation

<120> Recombinant BCG Strains Expressing Alanine Dehydrogenase,
Serine dehydratase and/or Glutamine Synthetase as TB Vaccines

<130>

<150> US 60/372,450

<151> 2002-04-16

<160> 14

<170> PatentIn version 3.0

<210> 1

<211> 1116

<212> DNA

<213> Mycobacterium tuberculosis

<220>

<221> CDS

<222> (1)..(1116)

<223> Sequence is identical to GenBank entries GI:3089350 and MTU92472

<400> 1

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gcc	atc	acc	ccg	gcc	ggc	gtc	gcg	gaa	cta	acc	cgt	cgt	ggc	cat	gag	96
Ala	Ile	Thr	Pro	Ala	Gly	Val	Ala	Glu	Leu	Thr	Arg	Arg	Gly	His	Glu	
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gtg	ctc	atc	cag	gca	ggt	gcc	gga	gag	ggc	tcg	gct	atc	acc	gac	gcg	144
Val	Leu	Ile	Gln	Ala	Gly	Ala	Gly	Glu	Gly	Ser	Ala	Ile	Thr	Asp	Ala	
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gat	ttc	aag	gcg	gca	ggc	gcg	caa	ctg	gtc	ggc	acc	gcc	gac	cag	gtg	192
Asp	Phe	Lys	Ala	Ala	Gly	Ala	Gln	Leu	Val	Gly	Thr	Ala	Asp	Gln	Val	
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tgg	gcc	gac	gct	gat	tta	ttg	ctc	aag	gtc	aaa	gaa	ccg	ata	gcg	gcg	240
Trp	Ala	Asp	Ala	Asp	Leu	Leu	Leu	Lys	Val	Lys	Glu	Pro	Ile	Ala	Ala	
65				70					75					80		

gaa	tac	ggc	cgc	ctg	cga	cac	ggg	cag	atc	ttg	ttc	acg	ttc	ttg	cat	288
Glu	Tyr	Gly	Arg	Leu	Arg	His	Gly	Gln	Ile	Leu	Phe	Thr	Phe	Leu	His	
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ttg	gcc	gcg	tca	cgt	gct	tgc	acc	gat	gcg	ttg	ttg	gat	tcc	ggc	acc	336
Leu	Ala	Ala	Ser	Arg	Ala	Cys	Thr	Asp	Ala	Leu	Leu	Asp	Ser	Gly	Thr	
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acg	tca	att	gcc	tac	gag	acc	gtc	cag	acc	gcc	gac	ggc	gca	cta	ccc	384
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Thr	Ser	Ile	Ala	Tyr	Glu	Thr	Val	Gln	Thr	Ala	Asp	Gly	Ala	Leu	Pro		
		115					120					125					
ctg	ctt	gcc	ccg	atg	agc	gaa	gtc	gcc	ggg	cga	ctc	gcc	gcc	cag	gtt	432	
Leu	Leu	Ala	Pro	Met	Ser	Glu	Val	Ala	Gly	Arg	Leu	Ala	Ala	Gln	Val		
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ggc	gct	tac	cac	ctg	atg	cga	acc	caa	ggg	ggc	cgc	ggg	gtg	ctg	atg	480	
Gly	Ala	Tyr	His	Leu	Met	Arg	Thr	Gln	Gly	Gly	Arg	Gly	Val	Leu	Met		
145					150					155					160		
ggc	ggg	gtg	ccc	ggc	gtc	gaa	ccg	gcc	gac	gtc	gtg	gtg	atc	ggc	gcc	528	
Gly	Gly	Val	Pro	Gly	Val	Glu	Pro	Ala	Asp	Val	Val	Val	Ile	Gly	Ala		
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ggc	acc	gcc	ggc	tac	aac	gca	gcc	cgc	atc	gcc	aac	ggc	atg	ggc	gcg	576	
Gly	Thr	Ala	Gly	Tyr	Asn	Ala	Ala	Arg	Ile	Ala	Asn	Gly	Met	Gly	Ala		
			180					185					190				
acc	gtt	acg	gtt	cta	gac	atc	aac	atc	gac	aaa	ctt	cgg	caa	ctc	gac	624	
Thr	Val	Thr	Val	Leu	Asp	Ile	Asn	Ile	Asp	Lys	Leu	Arg	Gln	Leu	Asp		
			195				200					205					
gcc	gag	ttc	tgc	ggc	cgg	atc	cac	act	cgc	tac	tca	tcg	gcc	tac	gag	672	
Ala	Glu	Phe	Cys	Gly	Arg	Ile	His	Thr	Arg	Tyr	Ser	Ser	Ala	Tyr	Glu		
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ctc	gag	ggg	gcc	gtc	aaa	cgt	gcc	gac	ctg	gtg	att	ggg	gcc	gtc	ctg	720	
Leu	Glu	Gly	Ala	Val	Lys	Arg	Ala	Asp	Leu	Val	Ile	Gly	Ala	Val	Leu		
225					230					235					240		
gtg	cca	ggc	gcc	aag	gca	ccc	aaa	tta	gtc	tcg	aat	tca	ctt	gtc	gcg	768	
Val	Pro	Gly	Ala	Lys	Ala	Pro	Lys	Leu	Val	Ser	Asn	Ser	Leu	Val	Ala		
				245					250					255			
cat	atg	aaa	cca	ggg	gcg	gta	ctg	gtg	gat	ata	gcc	atc	gac	cag	ggc	816	
His	Met	Lys	Pro	Gly	Ala	Val	Leu	Val	Asp	Ile	Ala	Ile	Asp	Gln	Gly		
			260				265						270				
ggc	tgt	ttc	gaa	ggc	tca	cga	ccg	acc	acc	tac	gac	cac	ccg	acg	ttc	864	
Gly	Cys	Phe	Glu	Gly	Ser	Arg	Pro	Thr	Thr	Tyr	Asp	His	Pro	Thr	Phe		
		275					280					285					
gcc	gtg	cac	gac	acg	ctg	ttt	tac	tgc	gtg	gcg	aac	atg	ccc	gcc	tcg	912	
Ala	Val	His	Asp	Thr	Leu	Phe	Tyr	Cys	Val	Ala	Asn	Met	Pro	Ala	Ser		
	290					295					300						
gtg	ccg	aag	acg	tcg	acc	tac	gcg	ctg	acc	aac	gcg	acg	atg	ccg	tat	960	
Val	Pro	Lys	Thr	Ser	Thr	Tyr	Ala	Leu	Thr	Asn	Ala	Thr	Met	Pro	Tyr		
305					310					315					320		
gtg	ctc	gag	ctt	gcc	gac	cat	ggc	tgg	cgg	gcg	gcg	tgc	cgg	tcg	aat	1008	
Val	Leu	Glu	Leu	Ala	Asp	His	Gly	Trp	Arg	Ala	Ala	Cys	Arg	Ser	Asn		
				325					330					335			
ccg	gca	cta	gcc	aaa	ggg	ctt	tcg	acg	cac	gaa	ggg	gcg	tta	ctg	tcc	1056	
Pro	Ala	Leu	Ala	Lys	Gly	Leu	Ser	Thr	His	Glu	Gly	Ala	Leu	Leu	Ser		

340 345 350
 gaa cgg gtg gcc acc gac ctg ggg gtg ccg ttc acc gag ccc gcc agc 1104
 Glu Arg Val Ala Thr Asp Leu Gly Val Pro Phe Thr Glu Pro Ala Ser
 355 360 365

 gtg ctg gcc tga 1116
 Val Leu Ala
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 <210> 2
 <211> 371
 <212> PRT
 <213> Mycobacterium tuberculosis

 <220>
 <221>
 <222>
 <223> Sequence is identical to SwissProt entry SP:DHA_MYCTU

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 Ala Ile Thr Pro Ala Gly Val Ala Glu Leu Thr Arg Arg Gly His Glu
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 Val Leu Ile Gln Ala Gly Ala Gly Glu Gly Ser Ala Ile Thr Asp Ala
 35 40 45

 Asp Phe Lys Ala Ala Gly Ala Gln Leu Val Gly Thr Ala Asp Gln Val
 50 55 60

 Trp Ala Asp Ala Asp Leu Leu Leu Lys Val Lys Glu Pro Ile Ala Ala
 65 70 75 80

 Glu Tyr Gly Arg Leu Arg His Gly Gln Ile Leu Phe Thr Phe Leu His
 85 90 95

 Leu Ala Ala Ser Arg Ala Cys Thr Asp Ala Leu Leu Asp Ser Gly Thr
 100 105 110

 Thr Ser Ile Ala Tyr Glu Thr Val Gln Thr Ala Asp Gly Ala Leu Pro
 115 120 125

 Leu Leu Ala Pro Met Ser Glu Val Ala Gly Arg Leu Ala Ala Gln Val
 130 135 140

Gly Ala Tyr His Leu Met Arg Thr Gln Gly Gly Arg Gly Val Leu Met
145 150 155 160

Gly Gly Val Pro Gly Val Glu Pro Ala Asp Val Val Val Ile Gly Ala
165 170 175

Gly Thr Ala Gly Tyr Asn Ala Ala Arg Ile Ala Asn Gly Met Gly Ala
180 185 190

Thr Val Thr Val Leu Asp Ile Asn Ile Asp Lys Leu Arg Gln Leu Asp
195 200 205

Ala Glu Phe Cys Gly Arg Ile His Thr Arg Tyr Ser Ser Ala Tyr Glu
210 215 220

Leu Glu Gly Ala Val Lys Arg Ala Asp Leu Val Ile Gly Ala Val Leu
225 230 235 240

Val Pro Gly Ala Lys Ala Pro Lys Leu Val Ser Asn Ser Leu Val Ala
245 250 255

His Met Lys Pro Gly Ala Val Leu Val Asp Ile Ala Ile Asp Gln Gly
260 265 270

Gly Cys Phe Glu Gly Ser Arg Pro Thr Thr Tyr Asp His Pro Thr Phe
275 280 285

Ala Val His Asp Thr Leu Phe Tyr Cys Val Ala Asn Met Pro Ala Ser
290 295 300

Val Pro Lys Thr Ser Thr Tyr Ala Leu Thr Asn Ala Thr Met Pro Tyr
305 310 315 320

Val Leu Glu Leu Ala Asp His Gly Trp Arg Ala Ala Cys Arg Ser Asn
325 330 335

Pro Ala Leu Ala Lys Gly Leu Ser Thr His Glu Gly Ala Leu Leu Ser
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Glu Arg Val Ala Thr Asp Leu Gly Val Pro Phe Thr Glu Pro Ala Ser
355 360 365

Val Leu Ala
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<210> 3
<211> 399
<212> DNA
<213> Mycobacterium bovis

<220>
<221> CDS
<222> (1)..(399)

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gcc atc acc ccg gcc ggc gtc gcg gaa cta acc cgt cgt ggc cat gag 96
Ala Ile Thr Pro Ala Gly Val Ala Glu Leu Thr Arg Arg Gly His Glu
20 25 30
gtg ctc atc cag gca ggt gcc gga gag ggc tcg gct atc acc gac gcg 144
Val Leu Ile Gln Ala Gly Ala Gly Glu Gly Ser Ala Ile Thr Asp Ala
35 40 45
gat ttc aag gcg gca ggc gcg caa ctg gtc ggc acc gcc gac cag gtg 192
Asp Phe Lys Ala Ala Gly Ala Gln Leu Val Gly Thr Ala Asp Gln Val
50 55 60
tgg gcc gac gct gat tta ttg ctc aag gtc aaa gaa ccg ata gcg gcg 240
Trp Ala Asp Ala Asp Leu Leu Leu Lys Val Lys Glu Pro Ile Ala Ala
65 70 75 80
gaa tac ggc cgc ctg cga cac ggg cga tct tgt tca cgt tct tgc att 288
Glu Tyr Gly Arg Leu Arg His Gly Arg Ser Cys Ser Arg Ser Cys Ile
85 90 95
tgg ccg cgt cac gtg ctt gca ccg atg cgt tgt tgg att ccg gca cca 336
Trp Pro Arg His Val Leu Ala Pro Met Arg Cys Trp Ile Pro Ala Pro
100 105 110
cgt caa ttg cct acg aga ccg tcc aga ccg ccg acg gcg cac tac ccc 384
Arg Gln Leu Pro Thr Arg Pro Ser Arg Pro Pro Thr Ala His Tyr Pro
115 120 125
tgc ttg ccc cga tga 399
Cys Leu Pro Arg
130

<210> 4
<211> 132
<212> PRT
<213> Mycobacterium bovis

<400> 4

Met Arg Val Gly Ile Pro Thr Glu Thr Lys Asn Asn Glu Phe Arg Val
1 5 10 15

Ala Ile Thr Pro Ala Gly Val Ala Glu Leu Thr Arg Arg Gly His Glu
20 25 30

Val Leu Ile Gln Ala Gly Ala Gly Glu Gly Ser Ala Ile Thr Asp Ala
35 40 45

Asp Phe Lys Ala Ala Gly Ala Gln Leu Val Gly Thr Ala Asp Gln Val
50 55 60

Trp Ala Asp Ala Asp Leu Leu Lys Val Lys Glu Pro Ile Ala Ala
65 70 75 80

Glu Tyr Gly Arg Leu Arg His Gly Arg Ser Cys Ser Arg Ser Cys Ile
85 90 95

Trp Pro Arg His Val Leu Ala Pro Met Arg Cys Trp Ile Pro Ala Pro
100 105 110

Arg Gln Leu Pro Thr Arg Pro Ser Arg Pro Pro Thr Ala His Tyr Pro
115 120 125

Cys Leu Pro Arg
130

<210> 5
<211> 1386
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<221> CDS
<222> (1)..(1386)
<223> Sequence is identical to the complement of nucleotides 13172-14551
of GenBank entry GB:MTV030 [AL021428]
Sequence is identical to the complement of nucleotides 13195-14580
of GenBank entry GB:AE006919

<400> 5
atg acc atc agc gtc ttc gac ctg ttc acc atc ggc atc ggg ccg tcc 48
Met Thr Ile Ser Val Phe Asp Leu Phe Thr Ile Gly Ile Gly Pro Ser
1 5 10 15

agt tcc cac acc gtg gga ccg atg cgc gcg gca aac cag ttc gta gtt 96
Ser Ser His Thr Val Gly Pro Met Arg Ala Ala Asn Gln Phe Val Val

20	25	30	
gcg ctg cgc cgc cgg ggc cac ctg gat gac ctc gag gcg atg cga gtg Ala Leu Arg Arg Arg Gly His Leu Asp Asp Leu Glu Ala Met Arg Val 35 40 45			144
gat ctg ttc ggc tcg ctc gcg gcc acc gga gcc ggt cat ggc acc atg Asp Leu Phe Gly Ser Leu Ala Ala Thr Gly Ala Gly His Gly Thr Met 50 55 60			192
tcg gcg ata ttg ctg ggg ctg gaa ggc tgc cag cca gaa acg att acc Ser Ala Ile Leu Leu Gly Leu Glu Gly Cys Gln Pro Glu Thr Ile Thr 65 70 75 80			240
acc gaa cac aag gaa cgc cgg ctc gcc gag atc gca gcg tcc ggc gtg Thr Glu His Lys Glu Arg Arg Leu Ala Glu Ile Ala Ala Ser Gly Val 85 90 95			288
acg cga atc ggc ggt gtc att ccg gtc ccg ctg acc gag cgt gat atc Thr Arg Ile Gly Gly Val Ile Pro Val Pro Leu Thr Glu Arg Asp Ile 100 105 110			336
gac ctg cat ccc gac atc gtt ctg cca acg cat ccc aac gga atg acg Asp Leu His Pro Asp Ile Val Leu Pro Thr His Pro Asn Gly Met Thr 115 120 125			384
ttc act gcc gcg ggc cca cac ggc cgc gtc ttg gcc acc gag act tat Phe Thr Ala Ala Gly Pro His Gly Arg Val Leu Ala Thr Glu Thr Tyr 130 135 140			432
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agc ggc caa cat cca tgc tca gtt gcc ctt ccc tac gtg tcg gcc caa Ser Gly Gln His Pro Cys Ser Val Ala Leu Pro Tyr Val Ser Ala Gln 165 170 175			528
gaa ctg ctg gac atc tgt gac cgc ctc gac gtg tca att agc gaa gcg Glu Leu Leu Asp Ile Cys Asp Arg Leu Asp Val Ser Ile Ser Glu Ala 180 185 190			576
gcg ctg cgc aac gaa aca tgt tgc cgc acc gag aac gag gta cgc gcc Ala Leu Arg Asn Glu Thr Cys Cys Arg Thr Glu Asn Glu Val Arg Ala 195 200 205			624
gcg ctg ctg cac ctg cgc gac gtc atg gtt gag tgc gaa cag cgg agc Ala Leu Leu His Leu Arg Asp Val Met Val Glu Cys Glu Gln Arg Ser 210 215 220			672
atc gct cgc gaa ggg ttg ctt cct ggc ggc ctc cgg gtg cgc cgg cga Ile Ala Arg Glu Gly Leu Leu Pro Gly Gly Leu Arg Val Arg Arg Arg 225 230 235 240			720
gcg aag gtg tgg tat gac cgc ttg aac gcc gaa gac ccc act cgc aag Ala Lys Val Trp Tyr Asp Arg Leu Asn Ala Glu Asp Pro Thr Arg Lys 245 250 255			768

ccg gaa ttc gct gag gac tgg gtc aac ctg gtc gcg ctg gca gtc aac Pro Glu Phe Ala Glu Asp Trp Val Asn Leu Val Ala Leu Ala Val Asn 260 265 270	816
gag gag aac gcc tcc ggt ggg cgc gtc gtc acc gcc ccg acc aac ggt Glu Glu Asn Ala Ser Gly Gly Arg Val Val Thr Ala Pro Thr Asn Gly 275 280 285	864
gcc gcc ggc atc gtg ccg gcg gtc ctg cac tac gca atc cac tac acg Ala Ala Gly Ile Val Pro Ala Val Leu His Tyr Ala Ile His Tyr Thr 290 295 300	912
tcg gcc ggc gcg ggg gac ccc gac gat gtc acc gtg cga ttc ctg ctc Ser Ala Gly Ala Gly Asp Pro Asp Asp Val Thr Val Arg Phe Leu Leu 305 310 315 320	960
act gct gga gcc atc gga tcg ttg ttc aag gag cga gca tcg atc tcc Thr Ala Gly Ala Ile Gly Ser Leu Phe Lys Glu Arg Ala Ser Ile Ser 325 330 335	1008
gga gcc gag gtc ggc tgt cag ggc gag gtc ggc tcc gcg gcc gcc atg Gly Ala Glu Val Gly Cys Gln Gly Glu Val Gly Ser Ala Ala Ala Met 340 345 350	1056
gcc gcc gcc gga ttg gct gaa atc ctc ggc ggc aca ccg cga caa gtg Ala Ala Ala Gly Leu Ala Glu Ile Leu Gly Gly Thr Pro Arg Gln Val 355 360 365	1104
gaa aac gcc gcc gag atc gcc atg gaa cac agc ctc ggc ctg acc tgt Glu Asn Ala Ala Glu Ile Ala Met Glu His Ser Leu Gly Leu Thr Cys 370 375 380	1152
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att tcc gcc ggc aag gcc atc aac gcc gca cgg atg gca ttg cgc ggc Ile Ser Ala Gly Lys Ala Ile Asn Ala Ala Arg Met Ala Leu Arg Gly 405 410 415	1248
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gcc acc ggc gcg gac atg cac acc aag tac aag gaa acc tcg gcc ggc Ala Thr Gly Ala Asp Met His Thr Lys Tyr Lys Glu Thr Ser Ala Gly 435 440 445	1344
ggg ctc gcc atc aac gtc gca gtc aac atc gtc gag tgt tga Gly Leu Ala Ile Asn Val Ala Val Asn Ile Val Glu Cys 450 455 460	1386

<210> 6
 <211> 461
 <212> PRT

<213> Mycobacterium tuberculosis

<220>

<221>

<222>

<223> Sequence is identical to SwissProt entry SP:SDHL_MYCTU
Sequence is identical to GenBank entries GP:AE006919_13
and GP:MTV030_11

<400> 6

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Ser Ser His Thr Val Gly Pro Met Arg Ala Ala Asn Gln Phe Val Val
20 25 30

Ala Leu Arg Arg Arg Gly His Leu Asp Asp Leu Glu Ala Met Arg Val
35 40 45

Asp Leu Phe Gly Ser Leu Ala Ala Thr Gly Ala Gly His Gly Thr Met
50 55 60

Ser Ala Ile Leu Leu Gly Leu Glu Gly Cys Gln Pro Glu Thr Ile Thr
65 70 75 80

Thr Glu His Lys Glu Arg Arg Leu Ala Glu Ile Ala Ala Ser Gly Val
85 90 95

Thr Arg Ile Gly Gly Val Ile Pro Val Pro Leu Thr Glu Arg Asp Ile
100 105 110

Asp Leu His Pro Asp Ile Val Leu Pro Thr His Pro Asn Gly Met Thr
115 120 125

Phe Thr Ala Ala Gly Pro His Gly Arg Val Leu Ala Thr Glu Thr Tyr
130 135 140

Phe Ser Val Gly Gly Gly Phe Ile Val Thr Glu Gln Thr Ser Gly Asn
145 150 155 160

Ser Gly Gln His Pro Cys Ser Val Ala Leu Pro Tyr Val Ser Ala Gln
165 170 175

Glu Leu Leu Asp Ile Cys Asp Arg Leu Asp Val Ser Ile Ser Glu Ala
180 185 190

Ala Leu Arg Asn Glu Thr Cys Cys Arg Thr Glu Asn Glu Val Arg Ala
 195 200 205

Ala Leu Leu His Leu Arg Asp Val Met Val Glu Cys Glu Gln Arg Ser
 210 215 220

Ile Ala Arg Glu Gly Leu Leu Pro Gly Gly Leu Arg Val Arg Arg Arg
 225 230 235 240

Ala Lys Val Trp Tyr Asp Arg Leu Asn Ala Glu Asp Pro Thr Arg Lys
 245 250 255

Pro Glu Phe Ala Glu Asp Trp Val Asn Leu Val Ala Leu Ala Val Asn
 260 265 270

Glu Glu Asn Ala Ser Gly Gly Arg Val Val Thr Ala Pro Thr Asn Gly
 275 280 285

Ala Ala Gly Ile Val Pro Ala Val Leu His Tyr Ala Ile His Tyr Thr
 290 295 300

Ser Ala Gly Ala Gly Asp Pro Asp Asp Val Thr Val Arg Phe Leu Leu
 305 310 315 320

Thr Ala Gly Ala Ile Gly Ser Leu Phe Lys Glu Arg Ala Ser Ile Ser
 325 330 335

Gly Ala Glu Val Gly Cys Gln Gly Glu Val Gly Ser Ala Ala Ala Met
 340 345 350

Ala Ala Ala Gly Leu Ala Glu Ile Leu Gly Gly Thr Pro Arg Gln Val
 355 360 365

Glu Asn Ala Ala Glu Ile Ala Met Glu His Ser Leu Gly Leu Thr Cys
 370 375 380

Asp Pro Ile Ala Gly Leu Val Gln Ile Pro Cys Ile Glu Arg Asn Ala
 385 390 395 400

Ile Ser Ala Gly Lys Ala Ile Asn Ala Ala Arg Met Ala Leu Arg Gly
 405 410 415

Asp Gly Ile His Arg Val Thr Leu Asp Gln Val Ile Asp Thr Met Arg
 420 425 430

Ala Thr Gly Ala Asp Met His Thr Lys Tyr Lys Glu Thr Ser Ala Gly
 435 440 445

Gly Leu Ala Ile Asn Val Ala Val Asn Ile Val Glu Cys
 450 455 460

<210> 7

<211> 1437

<212> DNA

<213> Mycobacterium tuberculosis

<220>

<221> CDS

<222> (1)..(1437)

<223> Sequence is identical to GenBank entry GB:MTU87280 [U87280]

Sequence is identical to nucleotides 163-1599 of GenBank
 entry GB:MTCY427 [Z70692]

Sequence is identical to nucleotides 93-1529 of GenBank entry GB:AE00707

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aag gtc gaa tat gtc gac gtc cgg ttc tgt gac ctg cct ggc atc atg 96
 Lys Val Glu Tyr Val Asp Val Arg Phe Cys Asp Leu Pro Gly Ile Met
 20 25 30

cag cac ttc acg att ccg gct tcg gcc ttt gac aag agc gtg ttt gac 144
 Gln His Phe Thr Ile Pro Ala Ser Ala Phe Asp Lys Ser Val Phe Asp
 35 40 45

gac ggc ttg gcc ttt gac ggc tcg tcg att cgc ggg ttc cag tcg atc 192
 Asp Gly Leu Ala Phe Asp Gly Ser Ser Ile Arg Gly Phe Gln Ser Ile
 50 55 60

cac gaa tcc gac atg ttg ctt ctt ccc gat ccc gag acg gcg cgc atc 240
 His Glu Ser Asp Met Leu Leu Leu Pro Asp Pro Glu Thr Ala Arg Ile
 65 70 75 80

gac ccg ttc cgc gcg gcc aag acg ctg aat atc aac ttc ttt gtg cac 288
 Asp Pro Phe Arg Ala Ala Lys Thr Leu Asn Ile Asn Phe Phe Val His
 85 90 95

gac ccg ttc acc ctg gag ccg tac tcc cgc gac ccg cgc aac atc gcc 336
 Asp Pro Phe Thr Leu Glu Pro Tyr Ser Arg Asp Pro Arg Asn Ile Ala
 100 105 110

cgc aag gcc gag aac tac ctg atc agc act ggc atc gcc gac acc gca 384

Arg Lys Ala Glu Asn Tyr Leu Ile Ser Thr Gly Ile Ala Asp Thr Ala	
115 120 125	
tac ttc ggc gcc gag gcc gag ttc tac att ttc gat tcg gtg agc ttc	432
Tyr Phe Gly Ala Glu Ala Glu Phe Tyr Ile Phe Asp Ser Val Ser Phe	
130 135 140	
gac tcg cgc gcc aac ggc tcc ttc tac gag gtg gac gcc atc tcg ggg	480
Asp Ser Arg Ala Asn Gly Ser Phe Tyr Glu Val Asp Ala Ile Ser Gly	
145 150 155 160	
tgg tgg aac acc ggc gcg gcg acc gag gcc gac ggc agt ccc aac cgg	528
Trp Trp Asn Thr Gly Ala Ala Thr Glu Ala Asp Gly Ser Pro Asn Arg	
165 170 175	
ggc tac aag gtc cgc cac aag ggc ggg tat ttc cca gtg gcc ccc aac	576
Gly Tyr Lys Val Arg His Lys Gly Gly Tyr Phe Pro Val Ala Pro Asn	
180 185 190	
gac caa tac gtc gac ctg cgc gac aag atg ctg acc aac ctg atc aac	624
Asp Gln Tyr Val Asp Leu Arg Asp Lys Met Leu Thr Asn Leu Ile Asn	
195 200 205	
tcc ggc ttc atc ctg gag aag ggc cac cac gag gtg ggc agc ggc gga	672
Ser Gly Phe Ile Leu Glu Lys Gly His His Glu Val Gly Ser Gly Gly	
210 215 220	
cag gcc gag atc aac tac cag ttc aat tcg ctg ctg cac gcc gcc gac	720
Gln Ala Glu Ile Asn Tyr Gln Phe Asn Ser Leu Leu His Ala Ala Asp	
225 230 235 240	
gac atg cag ttg tac aag tac atc atc aag aac acc gcc tgg cag aac	768
Asp Met Gln Leu Tyr Lys Tyr Ile Ile Lys Asn Thr Ala Trp Gln Asn	
245 250 255	
ggc aaa acg gtc acg ttc atg ccc aag ccg ctg ttc ggc gac aac ggg	816
Gly Lys Thr Val Thr Phe Met Pro Lys Pro Leu Phe Gly Asp Asn Gly	
260 265 270	
tcc ggc atg cac tgt cat cag tcg ctg tgg aag gac ggg gcc ccg ctg	864
Ser Gly Met His Cys His Gln Ser Leu Trp Lys Asp Gly Ala Pro Leu	
275 280 285	
atg tac gac gag acg ggt tat gcc ggt ctg tcg gac acg gcc cgt cat	912
Met Tyr Asp Glu Thr Gly Tyr Ala Gly Leu Ser Asp Thr Ala Arg His	
290 295 300	
tac atc ggc gcc ctg tta cac cac gcg ccg tcg ctg ctg gcc ttc acc	960
Tyr Ile Gly Gly Leu Leu His His Ala Pro Ser Leu Leu Ala Phe Thr	
305 310 315 320	
aac ccg acg gtg aac tcc tac aag cgg ctg gtt ccc ggt tac gag gcc	1008
Asn Pro Thr Val Asn Ser Tyr Lys Arg Leu Val Pro Gly Tyr Glu Ala	
325 330 335	
ccg atc aac ctg gtc tat agc cag cgc aac cgg tcg gca tgc gtg cgc	1056
Pro Ile Asn Leu Val Tyr Ser Gln Arg Asn Arg Ser Ala Cys Val Arg	

340	345	350	
atc ccg atc acc ggc agc aac ccg aag gcc aag cgg ctg gag ttc cga			1104
Ile Pro Ile Thr Gly Ser Asn Pro Lys Ala Lys Arg Leu Glu Phe Arg			
355	360	365	
agc ccc gac tcg tcg ggc aac ccg tat ctg gcg ttc tcg gcc atg ctg			1152
Ser Pro Asp Ser Ser Gly Asn Pro Tyr Leu Ala Phe Ser Ala Met Leu			
370	375	380	
atg gca ggc ctg gac ggt atc aag aac aag atc gag ccg cag gcg ccc			1200
Met Ala Gly Leu Asp Gly Ile Lys Asn Lys Ile Glu Pro Gln Ala Pro			
385	390	395	400
gtc gac aag gat ctc tac gag ctg ccg ccg gaa gag gcc gcg agt atc			1248
Val Asp Lys Asp Leu Tyr Glu Leu Pro Pro Glu Glu Ala Ala Ser Ile			
	405	410	415
ccg cag act ccg acc cag ctg tca gat gtg atc gac cgt ctc gag gcc			1296
Pro Gln Thr Pro Thr Gln Leu Ser Asp Val Ile Asp Arg Leu Glu Ala			
	420	425	430
gac cac gaa tac ctc acc gaa gga ggg gtg ttc aca aac gac ctg atc			1344
Asp His Glu Tyr Leu Thr Glu Gly Gly Val Phe Thr Asn Asp Leu Ile			
	435	440	445
gag acg tgg atc agt ttc aag cgc gaa aac gag atc gag ccg gtc aac			1392
Glu Thr Trp Ile Ser Phe Lys Arg Glu Asn Glu Ile Glu Pro Val Asn			
	450	455	460
atc cgg ccg cat ccc tac gaa ttc gcg ctg tac tac gac gtt taa			1437
Ile Arg Pro His Pro Tyr Glu Phe Ala Leu Tyr Tyr Asp Val			
465	470	475	

<210> 8
 <211> 478
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <221>
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 <223> Sequence is identical to SwissProt entry SP:GLN1_MYCTU
 Sequence is identical to PIR entry PIR:H70775
 Sequence is identical to PRF entry PRF:2323405A

<400> 8
 Met Thr Glu Lys Thr Pro Asp Asp Val Phe Lys Leu Ala Lys Asp Glu
 1 5 10 15

Lys Val Glu Tyr Val Asp Val Arg Phe Cys Asp Leu Pro Gly Ile Met
 20 25 30

Gln His Phe Thr Ile Pro Ala Ser Ala Phe Asp Lys Ser Val Phe Asp

35	40	45
Asp Gly Leu Ala Phe Asp Gly Ser Ser Ile Arg Gly Phe Gln Ser Ile		
50	55	60
His Glu Ser Asp Met Leu Leu Leu Pro Asp Pro Glu Thr Ala Arg Ile		
65	70	75
Asp Pro Phe Arg Ala Ala Lys Thr Leu Asn Ile Asn Phe Phe Val His		
85	90	95
Asp Pro Phe Thr Leu Glu Pro Tyr Ser Arg Asp Pro Arg Asn Ile Ala		
100	105	110
Arg Lys Ala Glu Asn Tyr Leu Ile Ser Thr Gly Ile Ala Asp Thr Ala		
115	120	125
Tyr Phe Gly Ala Glu Ala Glu Phe Tyr Ile Phe Asp Ser Val Ser Phe		
130	135	140
Asp Ser Arg Ala Asn Gly Ser Phe Tyr Glu Val Asp Ala Ile Ser Gly		
145	150	155
Trp Trp Asn Thr Gly Ala Ala Thr Glu Ala Asp Gly Ser Pro Asn Arg		
165	170	175
Gly Tyr Lys Val Arg His Lys Gly Gly Tyr Phe Pro Val Ala Pro Asn		
180	185	190
Asp Gln Tyr Val Asp Leu Arg Asp Lys Met Leu Thr Asn Leu Ile Asn		
195	200	205
Ser Gly Phe Ile Leu Glu Lys Gly His His Glu Val Gly Ser Gly Gly		
210	215	220
Gln Ala Glu Ile Asn Tyr Gln Phe Asn Ser Leu Leu His Ala Ala Asp		
225	230	235
Asp Met Gln Leu Tyr Lys Tyr Ile Ile Lys Asn Thr Ala Trp Gln Asn		
245	250	255
Gly Lys Thr Val Thr Phe Met Pro Lys Pro Leu Phe Gly Asp Asn Gly		
260	265	270

Ser Gly Met His Cys His Gln Ser Leu Trp Lys Asp Gly Ala Pro Leu
 275 280 285

Met Tyr Asp Glu Thr Gly Tyr Ala Gly Leu Ser Asp Thr Ala Arg His
 290 295 300

Tyr Ile Gly Gly Leu Leu His His Ala Pro Ser Leu Leu Ala Phe Thr
 305 310 315 320

Asn Pro Thr Val Asn Ser Tyr Lys Arg Leu Val Pro Gly Tyr Glu Ala
 325 330 335

Pro Ile Asn Leu Val Tyr Ser Gln Arg Asn Arg Ser Ala Cys Val Arg
 340 345 350

Ile Pro Ile Thr Gly Ser Asn Pro Lys Ala Lys Arg Leu Glu Phe Arg
 355 360 365

Ser Pro Asp Ser Ser Gly Asn Pro Tyr Leu Ala Phe Ser Ala Met Leu
 370 375 380

Met Ala Gly Leu Asp Gly Ile Lys Asn Lys Ile Glu Pro Gln Ala Pro
 385 390 395 400

Val Asp Lys Asp Leu Tyr Glu Leu Pro Pro Glu Glu Ala Ala Ser Ile
 405 410 415

Pro Gln Thr Pro Thr Gln Leu Ser Asp Val Ile Asp Arg Leu Glu Ala
 420 425 430

Asp His Glu Tyr Leu Thr Glu Gly Gly Val Phe Thr Asn Asp Leu Ile
 435 440 445

Glu Thr Trp Ile Ser Phe Lys Arg Glu Asn Glu Ile Glu Pro Val Asn
 450 455 460

Ile Arg Pro His Pro Tyr Glu Phe Ala Leu Tyr Tyr Asp Val
 465 470 475

<210> 9
 <211> 1341
 <212> DNA

<213> Mycobacterium tuberculosis

<220>

<221> CDS

<222> (1) .. (1341)

<223> Sequence is identical to complement of nucleotides 4950-6290
of GenBank entry GB:MTCY427 [Z70692]

Sequence is identical to complement of nucleotides 4880-6220
of GenBank entry GB:AE007073

<400> 9

atg gac cga cag aag gaa ttc gtt ctt cgt acc ctg gaa gaa cgc gac	48
Met Asp Arg Gln Lys Glu Phe Val Leu Arg Thr Leu Glu Glu Arg Asp	
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atc cgc ttc gtc cgg ctg tgg ttc aca gac gtg ctc ggt ttc ctc aag	96
Ile Arg Phe Val Arg Leu Trp Phe Thr Asp Val Leu Gly Phe Leu Lys	
20 25 30	
tcg gtc gcc atc gcc cca gcc gaa ctc gag ggc gcc ttc gag gaa ggc	144
Ser Val Ala Ile Ala Pro Ala Glu Leu Glu Gly Ala Phe Glu Glu Gly	
35 40 45	
atc ggc ttc gac gga tcc tcg atc gag ggc ttt gcg cgg gtc tcg gaa	192
Ile Gly Phe Asp Gly Ser Ser Ile Glu Gly Phe Ala Arg Val Ser Glu	
50 55 60	
tcc gat acg gtg gcg cac ccg gac ccg tcg acc ttc cag gtg ctg ccc	240
Ser Asp Thr Val Ala His Pro Asp Pro Ser Thr Phe Gln Val Leu Pro	
65 70 75 80	
tgg gcc acc agt tcc ggc cac cac cac tca gcg cgg atg ttt tgc gac	288
Trp Ala Thr Ser Ser Gly His His His Ser Ala Arg Met Phe Cys Asp	
85 90 95	
atc acc atg ccg gac ggc tcg ccg tcg tgg gcg gac ccg cgg cac gtg	336
Ile Thr Met Pro Asp Gly Ser Pro Ser Trp Ala Asp Pro Arg His Val	
100 105 110	
ttg cgg cgg cag ctg acg aag gcc ggc gaa ctc ggc ttc tcc tgc tac	384
Leu Arg Arg Gln Leu Thr Lys Ala Gly Glu Leu Gly Phe Ser Cys Tyr	
115 120 125	
gtg cat ccc gaa atc gag ttc ttc ctg ctc aag ccc gga ccc gag gac	432
Val His Pro Glu Ile Glu Phe Phe Leu Leu Lys Pro Gly Pro Glu Asp	
130 135 140	
ggg tcg gtg ccc gtc ccg gtc gac aac gcc ggc tat ttc gac caa gcg	480
Gly Ser Val Pro Val Pro Val Asp Asn Ala Gly Tyr Phe Asp Gln Ala	
145 150 155 160	
gtg cac gac tcc gcc ttg aac ttt cgc cgc cac gcg atc gat gcc ctg	528
Val His Asp Ser Ala Leu Asn Phe Arg Arg His Ala Ile Asp Ala Leu	
165 170 175	
gaa ttc atg ggc atc tcg gtg gag ttc agc cat cac gaa ggc gca ccc	576

Glu	Phe	Met	Gly	Ile	Ser	Val	Glu	Phe	Ser	His	His	Glu	Gly	Ala	Pro	
			180					185					190			
ggc	cag	cag	gag	atc	gac	ctg	cgg	ttt	gcc	gac	gct	ctg	tcg	atg	gct	624
Gly	Gln	Gln	Glu	Ile	Asp	Leu	Arg	Phe	Ala	Asp	Ala	Leu	Ser	Met	Ala	
			195				200					205				
gac	aac	gtg	atg	acc	ttc	cgc	tac	gtc	atc	aaa	gaa	gtc	gcg	ctg	gaa	672
Asp	Asn	Val	Met	Thr	Phe	Arg	Tyr	Val	Ile	Lys	Glu	Val	Ala	Leu	Glu	
			210				215				220					
gag	ggc	gcc	cgg	gcg	tcg	ttc	atg	ccc	aag	cca	ttc	ggc	cag	cac	ccg	720
Glu	Gly	Ala	Arg	Ala	Ser	Phe	Met	Pro	Lys	Pro	Phe	Gly	Gln	His	Pro	
					230					235					240	
ggc	tcg	gcg	atg	cac	acc	cac	atg	agc	ctg	ttc	gag	ggt	gat	gtc	aac	768
Gly	Ser	Ala	Met	His	Thr	His	Met	Ser	Leu	Phe	Glu	Gly	Asp	Val	Asn	
				245				250						255		
gcg	ttc	cac	agc	gct	gat	gat	ccg	ctg	cag	ctg	tcg	gaa	gtg	ggt	aaa	816
Ala	Phe	His	Ser	Ala	Asp	Asp	Pro	Leu	Gln	Leu	Ser	Glu	Val	Gly	Lys	
				260				265					270			
tcg	ttc	atc	gcc	ggg	atc	ctg	gag	cac	gct	tgc	gag	atc	agc	gcg	gtc	864
Ser	Phe	Ile	Ala	Gly	Ile	Leu	Glu	His	Ala	Cys	Glu	Ile	Ser	Ala	Val	
			275				280					285				
aca	aat	cag	tgg	gtc	aac	tct	tac	aag	cgg	ctg	gtg	cag	ggc	ggc	gaa	912
Thr	Asn	Gln	Trp	Val	Asn	Ser	Tyr	Lys	Arg	Leu	Val	Gln	Gly	Gly	Glu	
			290				295				300					
gcg	ccc	acg	gcc	gcg	tcg	tgg	ggg	gcc	gcc	aac	cga	tcc	gcc	cta	gtg	960
Ala	Pro	Thr	Ala	Ala	Ser	Trp	Gly	Ala	Ala	Asn	Arg	Ser	Ala	Leu	Val	
					310					315					320	
cgg	gtg	ccg	atg	tac	acg	ccg	cac	aag	acc	tcg	tcg	cgg	cgg	gtc	gaa	1008
Arg	Val	Pro	Met	Tyr	Thr	Pro	His	Lys	Thr	Ser	Ser	Arg	Arg	Val	Glu	
				325					330					335		
gta	cgc	agc	cct	gat	tcg	gcg	tgc	aat	ccc	tat	ctg	aca	ttc	gcc	gtg	1056
Val	Arg	Ser	Pro	Asp	Ser	Ala	Cys	Asn	Pro	Tyr	Leu	Thr	Phe	Ala	Val	
			340					345					350			
ctg	ctg	gcc	gcg	gga	ttg	cgg	ggt	gta	gag	aag	ggt	tac	gtg	ctg	ggc	1104
Leu	Leu	Ala	Ala	Gly	Leu	Arg	Gly	Val	Glu	Lys	Gly	Tyr	Val	Leu	Gly	
			355				360					365				
ccg	cag	gcc	gag	gac	aac	gta	tgg	gac	ctc	aca	ccc	gag	gaa	cgc	cga	1152
Pro	Gln	Ala	Glu	Asp	Asn	Val	Trp	Asp	Leu	Thr	Pro	Glu	Glu	Arg	Arg	
			370				375				380					
gcg	atg	ggg	tac	cga	gaa	ttg	ccg	tcc	agt	ttg	gat	agt	gcg	ctg	cgc	1200
Ala	Met	Gly	Tyr	Arg	Glu	Leu	Pro	Ser	Ser	Leu	Asp	Ser	Ala	Leu	Arg	
					390					395					400	
gcc	atg	gag	gcc	tcc	gaa	ctc	gtc	gcg	gag	gcc	ttg	ggg	gag	cac	gtt	1248
Ala	Met	Glu	Ala	Ser	Glu	Leu	Val	Ala	Glu	Ala	Leu	Gly	Glu	His	Val	

405 410 415
 ttt gac ttt ttc ttg cgc aac aag cgc acg gag tgg gcg aac tac cgc 1296
 Phe Asp Phe Phe Leu Arg Asn Lys Arg Thr Glu Trp Ala Asn Tyr Arg
 420 425 430

agc cac gtc acg cca tac gag ctg cgc acc tac ctg tcg ctg tag 1341
 Ser His Val Thr Pro Tyr Glu Leu Arg Thr Tyr Leu Ser Leu
 435 440 445

<210> 10

<211> 446

<212> PRT

<213> Mycobacterium tuberculosis

<220>

<221>

<222>

<223> Sequence is identical to SwissProt entry SP:GLN2_MYCTU
 Sequence is identical to PIR entry PIR:B70776

<400> 10

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 1 5 10 15

Ile Arg Phe Val Arg Leu Trp Phe Thr Asp Val Leu Gly Phe Leu Lys
 20 25 30

Ser Val Ala Ile Ala Pro Ala Glu Leu Glu Gly Ala Phe Glu Glu Gly
 35 40 45

Ile Gly Phe Asp Gly Ser Ser Ile Glu Gly Phe Ala Arg Val Ser Glu
 50 55 60

Ser Asp Thr Val Ala His Pro Asp Pro Ser Thr Phe Gln Val Leu Pro
 65 70 75 80

Trp Ala Thr Ser Ser Gly His His His Ser Ala Arg Met Phe Cys Asp
 85 90 95

Ile Thr Met Pro Asp Gly Ser Pro Ser Trp Ala Asp Pro Arg His Val
 100 105 110

Leu Arg Arg Gln Leu Thr Lys Ala Gly Glu Leu Gly Phe Ser Cys Tyr
 115 120 125

Val His Pro Glu Ile Glu Phe Phe Leu Leu Lys Pro Gly Pro Glu Asp

130	135	140
Gly Ser Val Pro Val Pro Val Asp Asn Ala Gly Tyr Phe Asp Gln Ala		
145	150	155 160
Val His Asp Ser Ala Leu Asn Phe Arg Arg His Ala Ile Asp Ala Leu		
	165	170 175
Glu Phe Met Gly Ile Ser Val Glu Phe Ser His His Glu Gly Ala Pro		
	180	185 190
Gly Gln Gln Glu Ile Asp Leu Arg Phe Ala Asp Ala Leu Ser Met Ala		
	195	200 205
Asp Asn Val Met Thr Phe Arg Tyr Val Ile Lys Glu Val Ala Leu Glu		
	210	215 220
Glu Gly Ala Arg Ala Ser Phe Met Pro Lys Pro Phe Gly Gln His Pro		
	225	230 235 240
Gly Ser Ala Met His Thr His Met Ser Leu Phe Glu Gly Asp Val Asn		
	245	250 255
Ala Phe His Ser Ala Asp Asp Pro Leu Gln Leu Ser Glu Val Gly Lys		
	260	265 270
Ser Phe Ile Ala Gly Ile Leu Glu His Ala Cys Glu Ile Ser Ala Val		
	275	280 285
Thr Asn Gln Trp Val Asn Ser Tyr Lys Arg Leu Val Gln Gly Gly Glu		
	290	295 300
Ala Pro Thr Ala Ala Ser Trp Gly Ala Ala Asn Arg Ser Ala Leu Val		
	305	310 315 320
Arg Val Pro Met Tyr Thr Pro His Lys Thr Ser Ser Arg Arg Val Glu		
	325	330 335
Val Arg Ser Pro Asp Ser Ala Cys Asn Pro Tyr Leu Thr Phe Ala Val		
	340	345 350
Leu Leu Ala Ala Gly Leu Arg Gly Val Glu Lys Gly Tyr Val Leu Gly		
	355	360 365

Pro Gln Ala Glu Asp Asn Val Trp Asp Leu Thr Pro Glu Glu Arg Arg
 370 375 380

Ala Met Gly Tyr Arg Glu Leu Pro Ser Ser Leu Asp Ser Ala Leu Arg
 385 390 395 400

Ala Met Glu Ala Ser Glu Leu Val Ala Glu Ala Leu Gly Glu His Val
 405 410 415

Phe Asp Phe Phe Leu Arg Asn Lys Arg Thr Glu Trp Ala Asn Tyr Arg
 420 425 430

Ser His Val Thr Pro Tyr Glu Leu Arg Thr Tyr Leu Ser Leu
 435 440 445

<210> 11
 <211> 1353
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <221> CDS
 <222> (1)..(1353)
 <223> Sequence is identical to nucleotides 4871-6223
 of GenBank entry GB:MTCY180 [Z97193]
 Sequence is identical to nucleotides 7308-8660
 of GenBank entry GB:AE007049

<400> 11
 atg aca gcc aca ccg ctt gcc gcg gcc gcg atc gcc caa ttg gag gca 48
 Met Thr Ala Thr Pro Leu Ala Ala Ala Ile Ala Gln Leu Glu Ala
 1 5 10 15
 gag ggc gtc gac acc gtc atc ggc acc gtc gtg aac ccc gcc gga ctc 96
 Glu Gly Val Asp Thr Val Ile Gly Thr Val Val Asn Pro Ala Gly Leu
 20 25 30
 acc cag gcc aag acc gtg ccg ata cgc cgg acc aac aca ttc gcc aat 144
 Thr Gln Ala Lys Thr Val Pro Ile Arg Arg Thr Asn Thr Phe Ala Asn
 35 40 45
 cct ggc ctc ggc gcc agt ccg gtg tgg cat acc ttc tgt atc gac caa 192
 Pro Gly Leu Gly Ala Ser Pro Val Trp His Thr Phe Cys Ile Asp Gln
 50 55 60
 tgc agt att gca ttc acc gca gac atc agt gtg gtc ggc gat caa cgt 240
 Cys Ser Ile Ala Phe Thr Ala Asp Ile Ser Val Val Gly Asp Gln Arg
 65 70 75 80

ctc	cgc	atc	gat	ctg	tcc	gcc	ttg	cgc	atc	atc	ggc	gac	ggg	ttg	gcg	288
Leu	Arg	Ile	Asp	Leu	Ser	Ala	Leu	Arg	Ile	Ile	Gly	Asp	Gly	Leu	Ala	
				85					90					95		
tgg	gcg	ccc	gcc	ggg	ttc	ttc	gag	cag	gac	ggc	aca	ccg	gtc	ccc	gcc	336
Trp	Ala	Pro	Ala	Gly	Phe	Phe	Glu	Gln	Asp	Gly	Thr	Pro	Val	Pro	Ala	
			100					105					110			
tgc	agc	cga	gga	aca	ctg	agc	cgg	atc	gag	gcc	gcg	ctt	gct	gat	gcc	384
Cys	Ser	Arg	Gly	Thr	Leu	Ser	Arg	Ile	Glu	Ala	Ala	Leu	Ala	Asp	Ala	
		115					120					125				
ggc	atc	gac	gcg	gta	atc	ggc	cac	gaa	gtc	gaa	ttc	ctc	ttg	gtc	gac	432
Gly	Ile	Asp	Ala	Val	Ile	Gly	His	Glu	Val	Glu	Phe	Leu	Leu	Val	Asp	
	130					135					140					
gcg	gac	ggc	cag	cgg	ctg	cct	tcg	acg	ctg	tgg	gcg	cag	tac	ggg	gtc	480
Ala	Asp	Gly	Gln	Arg	Leu	Pro	Ser	Thr	Leu	Trp	Ala	Gln	Tyr	Gly	Val	
145					150					155					160	
gcc	ggg	gtg	ctc	gag	cac	gag	gcg	ttc	gtc	cgc	gat	gtc	aac	gcc	gcg	528
Ala	Gly	Val	Leu	Glu	His	Glu	Ala	Phe	Val	Arg	Asp	Val	Asn	Ala	Ala	
				165					170					175		
gca	acg	gca	gca	ggc	atc	gct	atc	gag	cag	ttc	cat	ccc	gaa	tac	ggg	576
Ala	Thr	Ala	Ala	Gly	Ile	Ala	Ile	Glu	Gln	Phe	His	Pro	Glu	Tyr	Gly	
			180					185					190			
gcc	aac	caa	ttc	gag	atc	tcg	tta	gcg	ccg	cag	ccg	ccg	gtc	gcg	gcc	624
Ala	Asn	Gln	Phe	Glu	Ile	Ser	Leu	Ala	Pro	Gln	Pro	Pro	Val	Ala	Ala	
		195					200					205				
gcc	gat	cag	ctg	gtg	ctg	acc	cgc	ctc	atc	atc	ggc	cgt	acc	gcc	cgc	672
Ala	Asp	Gln	Leu	Val	Leu	Thr	Arg	Leu	Ile	Ile	Gly	Arg	Thr	Ala	Arg	
	210					215					220					
cgg	cac	ggg	tta	cgc	gtg	agc	cta	tcg	cca	gcg	ccc	ttc	gcc	gga	agt	720
Arg	His	Gly	Leu	Arg	Val	Ser	Leu	Ser	Pro	Ala	Pro	Phe	Ala	Gly	Ser	
225					230					235					240	
atc	gga	tcc	ggg	gcc	cac	caa	cac	ttc	tcg	ctg	act	atg	tcg	gaa	ggg	768
Ile	Gly	Ser	Gly	Ala	His	Gln	His	Phe	Ser	Leu	Thr	Met	Ser	Glu	Gly	
				245					250					255		
atg	ctg	ttc	tcc	ggg	ggg	act	gga	gca	gct	ggc	atg	acc	tcg	gcc	ggg	816
Met	Leu	Phe	Ser	Gly	Gly	Thr	Gly	Ala	Ala	Gly	Met	Thr	Ser	Ala	Gly	
			260					265					270			
gag	gcc	gcg	gtg	gca	gga	gtg	ctt	cgc	gga	cta	ccg	gac	gcc	caa	ggc	864
Glu	Ala	Ala	Val	Ala	Gly	Val	Leu	Arg	Gly	Leu	Pro	Asp	Ala	Gln	Gly	
		275					280					285				
atc	ctg	tgc	gga	tcg	atc	gtg	tcc	ggg	ctg	cga	atg	cga	ccc	ggg	aac	912
Ile	Leu	Cys	Gly	Ser	Ile	Val	Ser	Gly	Leu	Arg	Met	Arg	Pro	Gly	Asn	
	290					295					300					
tgg	gcc	gga	atc	tat	gca	tgc	tgg	ggg	acc	gaa	aac	cgg	gaa	gcg	gcg	960

Trp	Ala	Gly	Ile	Tyr	Ala	Cys	Trp	Gly	Thr	Glu	Asn	Arg	Glu	Ala	Ala		
305					310					315					320		
gtg	cga	ttc	gtc	aag	ggc	ggg	gct	ggc	agc	gcg	tac	ggc	ggg	aac	gtg		1008
Val	Arg	Phe	Val	Lys	Gly	Gly	Ala	Gly	Ser	Ala	Tyr	Gly	Gly	Asn	Val		
				325					330					335			
gag	gtg	aag	gtc	gtc	gac	ccg	tcg	gcc	aac	ccg	tat	ctc	gcg	tcg	gcg		1056
Glu	Val	Lys	Val	Val	Asp	Pro	Ser	Ala	Asn	Pro	Tyr	Leu	Ala	Ser	Ala		
			340					345					350				
gcg	atc	ctc	gga	ctg	gca	ctc	gac	ggc	atg	aag	acc	aag	gcg	gtg	ttg		1104
Ala	Ile	Leu	Gly	Leu	Ala	Leu	Asp	Gly	Met	Lys	Thr	Lys	Ala	Val	Leu		
		355					360					365					
ccg	tcg	gaa	acg	acc	gta	gac	ccg	aca	cag	ctg	tct	gac	gtg	gat	cgt		1152
Pro	Ser	Glu	Thr	Thr	Val	Asp	Pro	Thr	Gln	Leu	Ser	Asp	Val	Asp	Arg		
	370					375					380						
gac	cgt	gcc	ggc	att	ctg	cga	ctt	gct	gcc	gat	cag	gcg	gat	gca	att		1200
Asp	Arg	Ala	Gly	Ile	Leu	Arg	Leu	Ala	Ala	Asp	Gln	Ala	Asp	Ala	Ile		
385					390				395					400			
gct	gta	ctg	gat	agt	tcg	aaa	ctg	ctt	cgg	tgc	atc	ctt	ggc	gat	ccc		1248
Ala	Val	Leu	Asp	Ser	Ser	Lys	Leu	Leu	Arg	Cys	Ile	Leu	Gly	Asp	Pro		
				405				410					415				
gtg	gta	gat	gcc	gtg	gtc	gcg	gta	cgc	cag	tta	gag	cat	gag	cgc	tac		1296
Val	Val	Asp	Ala	Val	Val	Ala	Val	Arg	Gln	Leu	Glu	His	Glu	Arg	Tyr		
			420				425				430						
ggt	gac	ctc	gat	cct	gcg	cag	ctg	gcc	gac	aag	ttc	cgg	atg	gct	tgg		1344
Gly	Asp	Leu	Asp	Pro	Ala	Gln	Leu	Ala	Asp	Lys	Phe	Arg	Met	Ala	Trp		
	435					440					445						
agt	gtg	taa															1353
Ser	Val																
450																	

<210> 12
 <211> 450
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <221>
 <222>
 <223> Sequence is identical to PIR entry PIR:C70515

<400> 12
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Glu Gly Val Asp Thr Val Ile Gly Thr Val Val Asn Pro Ala Gly Leu

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		35					40					45			
Pro	Gly	Leu	Gly	Ala	Ser	Pro	Val	Trp	His	Thr	Phe	Cys	Ile	Asp	Gln
	50					55					60				
Cys	Ser	Ile	Ala	Phe	Thr	Ala	Asp	Ile	Ser	Val	Val	Gly	Asp	Gln	Arg
65					70					75					80
Leu	Arg	Ile	Asp	Leu	Ser	Ala	Leu	Arg	Ile	Ile	Gly	Asp	Gly	Leu	Ala
				85					90					95	
Trp	Ala	Pro	Ala	Gly	Phe	Phe	Glu	Gln	Asp	Gly	Thr	Pro	Val	Pro	Ala
			100					105					110		
Cys	Ser	Arg	Gly	Thr	Leu	Ser	Arg	Ile	Glu	Ala	Ala	Leu	Ala	Asp	Ala
		115					120					125			
Gly	Ile	Asp	Ala	Val	Ile	Gly	His	Glu	Val	Glu	Phe	Leu	Leu	Val	Asp
	130					135					140				
Ala	Asp	Gly	Gln	Arg	Leu	Pro	Ser	Thr	Leu	Trp	Ala	Gln	Tyr	Gly	Val
145					150					155					160
Ala	Gly	Val	Leu	Glu	His	Glu	Ala	Phe	Val	Arg	Asp	Val	Asn	Ala	Ala
				165					170					175	
Ala	Thr	Ala	Ala	Gly	Ile	Ala	Ile	Glu	Gln	Phe	His	Pro	Glu	Tyr	Gly
			180					185					190		
Ala	Asn	Gln	Phe	Glu	Ile	Ser	Leu	Ala	Pro	Gln	Pro	Pro	Val	Ala	Ala
		195					200					205			
Ala	Asp	Gln	Leu	Val	Leu	Thr	Arg	Leu	Ile	Ile	Gly	Arg	Thr	Ala	Arg
	210					215					220				
Arg	His	Gly	Leu	Arg	Val	Ser	Leu	Ser	Pro	Ala	Pro	Phe	Ala	Gly	Ser
225					230					235					240
Ile	Gly	Ser	Gly	Ala	His	Gln	His	Phe	Ser	Leu	Thr	Met	Ser	Glu	Gly
				245					250					255	

Met Leu Phe Ser Gly Gly Thr Gly Ala Ala Gly Met Thr Ser Ala Gly
 260 265 270

Glu Ala Ala Val Ala Gly Val Leu Arg Gly Leu Pro Asp Ala Gln Gly
 275 280 285

Ile Leu Cys Gly Ser Ile Val Ser Gly Leu Arg Met Arg Pro Gly Asn
 290 295 300

Trp Ala Gly Ile Tyr Ala Cys Trp Gly Thr Glu Asn Arg Glu Ala Ala
 305 310 315 320

Val Arg Phe Val Lys Gly Gly Ala Gly Ser Ala Tyr Gly Gly Asn Val
 325 330 335

Glu Val Lys Val Val Asp Pro Ser Ala Asn Pro Tyr Leu Ala Ser Ala
 340 345 350

Ala Ile Leu Gly Leu Ala Leu Asp Gly Met Lys Thr Lys Ala Val Leu
 355 360 365

Pro Ser Glu Thr Thr Val Asp Pro Thr Gln Leu Ser Asp Val Asp Arg
 370 375 380

Asp Arg Ala Gly Ile Leu Arg Leu Ala Ala Asp Gln Ala Asp Ala Ile
 385 390 395 400

Ala Val Leu Asp Ser Ser Lys Leu Leu Arg Cys Ile Leu Gly Asp Pro
 405 410 415

Val Val Asp Ala Val Val Ala Val Arg Gln Leu Glu His Glu Arg Tyr
 420 425 430

Gly Asp Leu Asp Pro Ala Gln Leu Ala Asp Lys Phe Arg Met Ala Trp
 435 440 445

Ser Val
 450

<210> 13
 <211> 1374
 <212> DNA

<213> Mycobacterium tuberculosis

<220>

<221> CDS

<222> (1)..(1374)

<223> Sequence is identical to complement of nucleotides 3104-4477
of GenBank entry GB:MTV003 [AL008883]

Sequence is identical to complement of nucleotides 3138-4511
of GenBank entry GB:AE007117

<400> 13

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Met Thr Gly Pro Gly Ser Pro Pro Leu Ala Trp Thr Glu Leu Glu Arg	
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ctg gtc gcg gcc ggt gac gtc gac acc gtc atc gtc gcg ttc acc gac	96
Leu Val Ala Ala Gly Asp Val Asp Thr Val Ile Val Ala Phe Thr Asp	
20 25 30	
atg cag ggc cgg ctg gcc ggc aaa cgg ata tcg ggc cgg cat ttc gtc	144
Met Gln Gly Arg Leu Ala Gly Lys Arg Ile Ser Gly Arg His Phe Val	
35 40 45	
gac gac ata gcc acc cgc ggc gtc gag tgc tgc agt tat ctg ctg gcc	192
Asp Asp Ile Ala Thr Arg Gly Val Glu Cys Cys Ser Tyr Leu Leu Ala	
50 55 60	
gtg gac gtc gac ctg aac acg gtg ccc ggc tat gcg atg gcc agt tgg	240
Val Asp Val Asp Leu Asn Thr Val Pro Gly Tyr Ala Met Ala Ser Trp	
65 70 75 80	
gac acc ggc tac ggc gat atg gtg atg acg ccg gac ttg tcc act ctg	288
Asp Thr Gly Tyr Gly Asp Met Val Met Thr Pro Asp Leu Ser Thr Leu	
85 90 95	
cgg ctg att cct tgg cta ccg gga acg gcg ctg gtg atc gcc gac ctg	336
Arg Leu Ile Pro Trp Leu Pro Gly Thr Ala Leu Val Ile Ala Asp Leu	
100 105 110	
gtc tgg gcc gac ggc agc gag gtc gcc gtc tcg ccg cgc agc att ctg	384
Val Trp Ala Asp Gly Ser Glu Val Ala Val Ser Pro Arg Ser Ile Leu	
115 120 125	
cgc cgt cag ctc gat cgg ctc aag gcg cgc gga ctg gtc gcc gat gtg	432
Arg Arg Gln Leu Asp Arg Leu Lys Ala Arg Gly Leu Val Ala Asp Val	
130 135 140	
gcc acc gag ctg gag ttc atc gtg ttc gac cag ccg tat cgc cag gca	480
Ala Thr Glu Leu Glu Phe Ile Val Phe Asp Gln Pro Tyr Arg Gln Ala	
145 150 155 160	
tgg gcc agc ggg tat cgc ggg ctg acc ccg gcc agc gac tac aac atc	528
Trp Ala Ser Gly Tyr Arg Gly Leu Thr Pro Ala Ser Asp Tyr Asn Ile	
165 170 175	
gac tac gcg ata ttg gca tcc tcg cgg atg gag ccg ttg ctg cgc gac	576

Asp	Tyr	Ala	Ile	Leu	Ala	Ser	Ser	Arg	Met	Glu	Pro	Leu	Leu	Arg	Asp		
			180					185					190				
atc	cgg	ttg	ggt	atg	gcc	ggt	gcg	ggt	ctg	cga	ttc	gag	gcg	gtc	aaa	624	
Ile	Arg	Leu	Gly	Met	Ala	Gly	Ala	Gly	Leu	Arg	Phe	Glu	Ala	Val	Lys		
		195				200					205						
ggc	gaa	tgc	aac	atg	ggc	cag	cag	gag	atc	ggg	ttt	cgt	tac	gac	gag	672	
Gly	Glu	Cys	Asn	Met	Gly	Gln	Gln	Glu	Ile	Gly	Phe	Arg	Tyr	Asp	Glu		
	210				215					220							
gcg	ctg	gtc	acc	tgc	gac	aac	cat	gcg	atc	tac	aag	aac	ggc	gcc	aag	720	
Ala	Leu	Val	Thr	Cys	Asp	Asn	His	Ala	Ile	Tyr	Lys	Asn	Gly	Ala	Lys		
225					230					235					240		
gaa	atc	gcc	gac	cag	cac	ggc	aag	agc	cta	acg	ttc	atg	gcg	aaa	tac	768	
Glu	Ile	Ala	Asp	Gln	His	Gly	Lys	Ser	Leu	Thr	Phe	Met	Ala	Lys	Tyr		
			245						250					255			
gat	gaa	cgc	gaa	ggt	aat	agc	tgt	cac	atc	cat	gtc	tcg	ctg	cgt	ggc	816	
Asp	Glu	Arg	Glu	Gly	Asn	Ser	Cys	His	Ile	His	Val	Ser	Leu	Arg	Gly		
			260					265					270				
acg	gat	ggc	tcc	gcg	gtg	ttt	gcc	gac	agt	aac	ggg	ccg	cac	ggc	atg	864	
Thr	Asp	Gly	Ser	Ala	Val	Phe	Ala	Asp	Ser	Asn	Gly	Pro	His	Gly	Met		
	275						280					285					
tcg	tcg	atg	ttc	cgc	agc	ttc	gtc	gcc	ggc	cag	ttg	gcc	acg	ttg	cgc	912	
Ser	Ser	Met	Phe	Arg	Ser	Phe	Val	Ala	Gly	Gln	Leu	Ala	Thr	Leu	Arg		
	290					295					300						
gaa	ttc	acg	ctg	tgc	tat	gcg	ccg	acc	att	aac	tcc	tac	aag	cga	ttt	960	
Glu	Phe	Thr	Leu	Cys	Tyr	Ala	Pro	Thr	Ile	Asn	Ser	Tyr	Lys	Arg	Phe		
305					310					315					320		
gcc	gat	agc	agt	ttc	gcg	ccg	acg	gcg	ctg	gct	tgg	ggg	ctg	gac	aat	1008	
Ala	Asp	Ser	Ser	Phe	Ala	Pro	Thr	Ala	Leu	Ala	Trp	Gly	Leu	Asp	Asn		
				325					330					335			
cgc	acc	tgc	gcc	ctg	cgg	gtg	gtt	ggc	cac	ggg	caa	aac	atc	cgg	gtc	1056	
Arg	Thr	Cys	Ala	Leu	Arg	Val	Val	Gly	His	Gly	Gln	Asn	Ile	Arg	Val		
			340					345					350				
gaa	tgc	cgg	gtt	ccc	ggc	ggt	gat	gtc	aac	cag	tac	ctg	gcg	gtg	gcg	1104	
Glu	Cys	Arg	Val	Pro	Gly	Gly	Asp	Val	Asn	Gln	Tyr	Leu	Ala	Val	Ala		
	355					360						365					
gct	ctc	att	gct	gga	ggg	ttg	tac	ggt	atc	gag	cgg	ggc	ctt	cag	ctg	1152	
Ala	Leu	Ile	Ala	Gly	Gly	Leu	Tyr	Gly	Ile	Glu	Arg	Gly	Leu	Gln	Leu		
	370					375					380						
ccc	gag	ccc	tgt	gtc	ggc	aac	gcc	tac	caa	ggc	gcc	gat	gtc	gaa	cgg	1200	
Pro	Glu	Pro	Cys	Val	Gly	Asn	Ala	Tyr	Gln	Gly	Ala	Asp	Val	Glu	Arg		
385					390					395					400		
ctg	ccg	gtt	acg	ctg	gcc	gac	gcc	gcg	gtg	ctg	ttc	gag	gat	tct	gcg	1248	
Leu	Pro	Val	Thr	Leu	Ala	Asp	Ala	Ala	Val	Leu	Phe	Glu	Asp	Ser	Ala		

405 410 415
 ctg gtg cgc gag gcg ttc ggc gag gat gtt gtc gcg cac tac ctg aac 1296
 Leu Val Arg Glu Ala Phe Gly Glu Asp Val Val Ala His Tyr Leu Asn
 420 425 430
 aac gcg cgt gtg gag ctg gcg gcg ttc aac gcg gcg gtc acc gat tgg 1344
 Asn Ala Arg Val Glu Leu Ala Ala Phe Asn Ala Ala Val Thr Asp Trp
 435 440 445
 gag agg ata cgt gga ttt gag cgc ctc tag 1374
 Glu Arg Ile Arg Gly Phe Glu Arg Leu
 450 455

 <210> 14
 <211> 457
 <212> PRT
 <213> Mycobacterium tuberculosis

 <220>
 <221>
 <222>
 <223> Sequence is identical to PIR entry PIR:F70885

 <400> 14
 Met Thr Gly Pro Gly Ser Pro Pro Leu Ala Trp Thr Glu Leu Glu Arg
 1 5 10 15
 Leu Val Ala Ala Gly Asp Val Asp Thr Val Ile Val Ala Phe Thr Asp
 20 25 30
 Met Gln Gly Arg Leu Ala Gly Lys Arg Ile Ser Gly Arg His Phe Val
 35 40 45
 Asp Asp Ile Ala Thr Arg Gly Val Glu Cys Cys Ser Tyr Leu Leu Ala
 50 55 60
 Val Asp Val Asp Leu Asn Thr Val Pro Gly Tyr Ala Met Ala Ser Trp
 65 70 75 80
 Asp Thr Gly Tyr Gly Asp Met Val Met Thr Pro Asp Leu Ser Thr Leu
 85 90 95
 Arg Leu Ile Pro Trp Leu Pro Gly Thr Ala Leu Val Ile Ala Asp Leu
 100 105 110
 Val Trp Ala Asp Gly Ser Glu Val Ala Val Ser Pro Arg Ser Ile Leu
 115 120 125

Arg Arg Gln Leu Asp Arg Leu Lys Ala Arg Gly Leu Val Ala Asp Val
 130 135 140

Ala Thr Glu Leu Glu Phe Ile Val Phe Asp Gln Pro Tyr Arg Gln Ala
 145 150 155 160

Trp Ala Ser Gly Tyr Arg Gly Leu Thr Pro Ala Ser Asp Tyr Asn Ile
 165 170 175

Asp Tyr Ala Ile Leu Ala Ser Ser Arg Met Glu Pro Leu Leu Arg Asp
 180 185 190

Ile Arg Leu Gly Met Ala Gly Ala Gly Leu Arg Phe Glu Ala Val Lys
 195 200 205

Gly Glu Cys Asn Met Gly Gln Gln Glu Ile Gly Phe Arg Tyr Asp Glu
 210 215 220

Ala Leu Val Thr Cys Asp Asn His Ala Ile Tyr Lys Asn Gly Ala Lys
 225 230 235 240

Glu Ile Ala Asp Gln His Gly Lys Ser Leu Thr Phe Met Ala Lys Tyr
 245 250 255

Asp Glu Arg Glu Gly Asn Ser Cys His Ile His Val Ser Leu Arg Gly
 260 265 270

Thr Asp Gly Ser Ala Val Phe Ala Asp Ser Asn Gly Pro His Gly Met
 275 280 285

Ser Ser Met Phe Arg Ser Phe Val Ala Gly Gln Leu Ala Thr Leu Arg
 290 295 300

Glu Phe Thr Leu Cys Tyr Ala Pro Thr Ile Asn Ser Tyr Lys Arg Phe
 305 310 315 320

Ala Asp Ser Ser Phe Ala Pro Thr Ala Leu Ala Trp Gly Leu Asp Asn
 325 330 335

Arg Thr Cys Ala Leu Arg Val Val Gly His Gly Gln Asn Ile Arg Val
 340 345 350

Glu Cys Arg Val Pro Gly Gly Asp Val Asn Gln Tyr Leu Ala Val Ala
355 360 365

Ala Leu Ile Ala Gly Gly Leu Tyr Gly Ile Glu Arg Gly Leu Gln Leu
370 375 380

Pro Glu Pro Cys Val Gly Asn Ala Tyr Gln Gly Ala Asp Val Glu Arg
385 390 395 400

Leu Pro Val Thr Leu Ala Asp Ala Ala Val Leu Phe Glu Asp Ser Ala
405 410 415

Leu Val Arg Glu Ala Phe Gly Glu Asp Val Val Ala His Tyr Leu Asn
420 425 430

Asn Ala Arg Val Glu Leu Ala Ala Phe Asn Ala Ala Val Thr Asp Trp
435 440 445

Glu Arg Ile Arg Gly Phe Glu Arg Leu
450 455